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Display Show Send to Hide: ☐ Sequence ☐ Lesser featuresRange: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ STS☐ 1: NM_032995. Reports Homo sapiens Rho ...[gi:15011980]

Links

Comment Features Sequence

LOCUS NM_032995 4258 bp mRNA linear PRI 17-NOV-2006

DEFINITION Homo sapiens Rho guanine nucleotide exchange factor (GEF) 4 (ARHGEF4), transcript variant 2, mRNA.

ACCESSION NM_032995

VERSION NM_032995.1 GI:15011980

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4258)

AUTHORS Kawasaki,Y., Senda,T., Ishidate,T., Koyama,R., Morishita,T., Iwayama,Y., Higuchi,O. and Akiyama,T.

TITLE Asef, a link between the tumor suppressor APC and G-protein signaling

JOURNAL Science 289 (5482), 1194-1197 (2000)

PUBMED 10947987

REFERENCE 2 (bases 1 to 4258)

AUTHORS Thiesen,S., Kubart,S., Ropers,H.H. and Nothwang,H.G.

TITLE Isolation of two novel human RhoGEFs, ARHGEF3 and ARHGEF4, in 3p13-21 and 2q22

JOURNAL Biochem. Biophys. Res. Commun. 273 (1), 364-369 (2000)

PUBMED 10873612

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [AB029035.1](#) and [AF249745.1](#).

Summary: Rho GTPases play a fundamental role in numerous cellular processes that are initiated by extracellular stimuli that work through G protein coupled receptors. The encoded protein may form complex with G proteins and stimulate Rho-dependent signals. This protein is similar to rat collybistin protein. Alternative splicing of this gene generates two transcript variants which encode different isoforms. Also there is possibility for the usage of multiple polyadenylation sites for this gene.

Transcript Variant: This variant (2) has 591 additional bases in the coding region compared to variant 1. This causes the reading frame shift and an early termination. Isoform b encoded by this variant is thus 20 amino acids shorter than isoform a encoded by variant 1.

COMPLETENESS: full length.

FEATURES

source Location/Qualifiers

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gene 1..4258

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Sep 27 2006 15:22:06